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Fig.1.

10	20	30	40	
ATG GAG CGC TGC CCC AGC CTA GGG GTC ACC CTC TAC GCC CTG GTG				
M E R C P S L G V T L Y A L V>				
50	60	70	80	90
GTG GTC CTG GGG CTG CGG GCG ACA CCG GCC GGC GGC CAG CAC TAT				
V V L G L R A T P A G G G O H Y>				
100	110	120	130	
CTC CAC ATC CGC CCG GCA CCC AGC GAC AAC CTG CCC CTG GTG GAC				
L H I R P A P S D N L P L V D>				
140	150	160	170	180
CTC ATC GAA CAC CCA GAC CCT ATC TTT GAC CCC AAG GAA AAG GAT				
L I E H P D P I F D P K E K D>				
190	200	210	220	
CTG AAC GAG ACG CTG CTG CGC TCG CTG CTC GGG GGC CAC TAC GAC				
L N E T L L R S L L G G H Y D>				
230	240	250	260	270
CCA GGC TTC ATG GCC ACC TCG CCC CCC GAG GAC CGG CCC GGC GGG				
P G F M A T S P P E D R P G G>				
280	290	300	310	
GGC GGG GGT GCA GCT GGG GGC GCG GAG GAC CTG GGG GAG CTG GAC				
G G G A A G G A E D L A E L D>				
320	330	340	350	360
CAG CTG CTG CGG CAG CGG CGG TCG GGG GCC ATG CCG AGC GAG ATC				
Q L L R Q R P S G A M P S E I>				
370	380	390	400	
AAA GGG CTA GAG TTC TCC GAG GGC TTG GCC CAG GGC AAG AAG CAG				
K G L E F S E G L A Q G K K Q>				
410	420	430	440	450
CGC CTA AGC AAG AAG CTG CGG AGG AAG TTA CAG ATG TGG CTG TGG				
R L S K K L R R K L Q M W L W>				
460	470	480	490	
TCG CAG ACA TTC TGC CCC GTG CTG TAC GCG TGG AAC GAC CTG GGC				
S Q T F C P V L Y A W N D L G>				
500	510	520	530	540
AGC CGC TTT TGG CCG CGC TAC GTG AAG GTG GGC AGC TGC TTC AGT				
S R F W P R Y V K V G S C F S>				

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Fig.1. (cont.)

550            560            570            580 —  
AAG CGC TCG TGC TCC GTG CCC GAG GGC ATG GTG TGC AAG CCG TCC  
K R S C S V \*P E G M V C K P S>  
590            600            610            620            630  
AAG TCC GTG CAC CTC ACG GTG CTG CGG TGG CCC TGT CAG CGG CGC  
K S V H L T V L R W R C Q R R>  
640            650            660            670  
GGG GGC CAG CGC TGC GGC TGG ATT CCC ATC CAG TAC CCC ATC ATT  
G G Q R C G W I P I Q Y P I I>  
680            690  
TCC GAG TGC AAG TGC TCG TGC TAG  
S E C K C S C \*>

Fig. 2A.

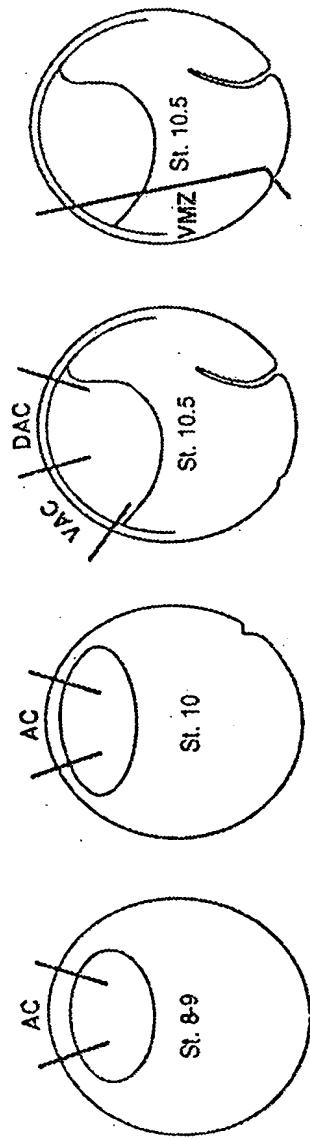


Fig. 2B.

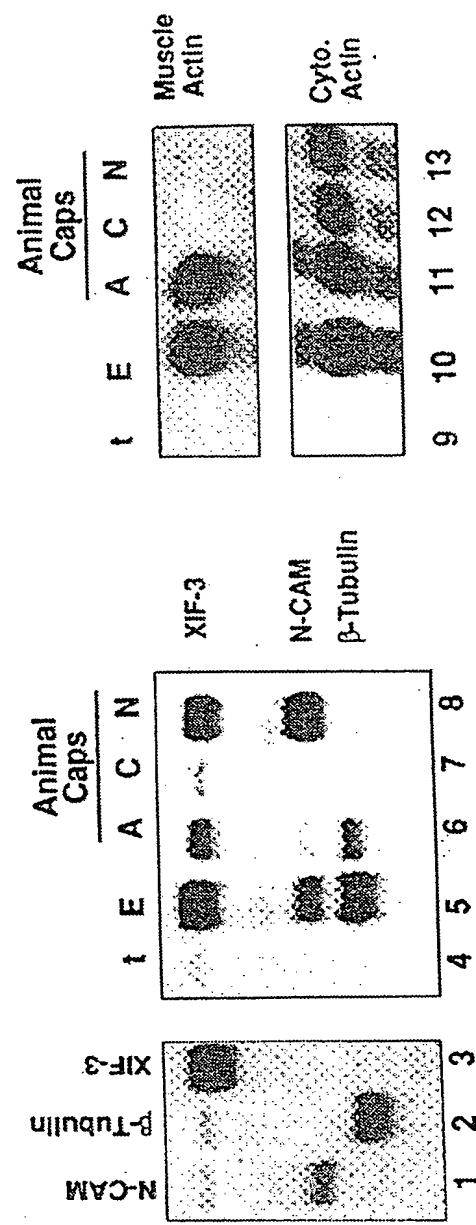
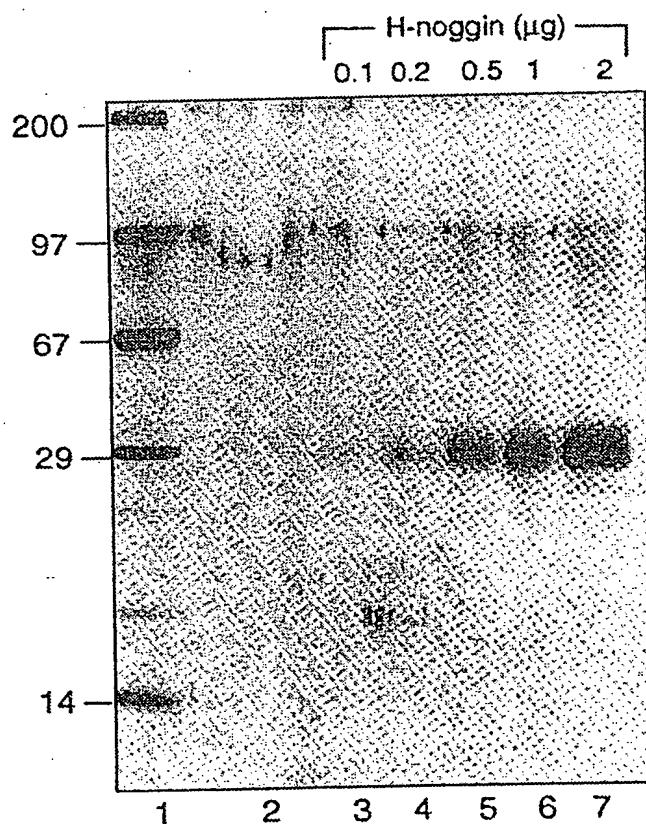


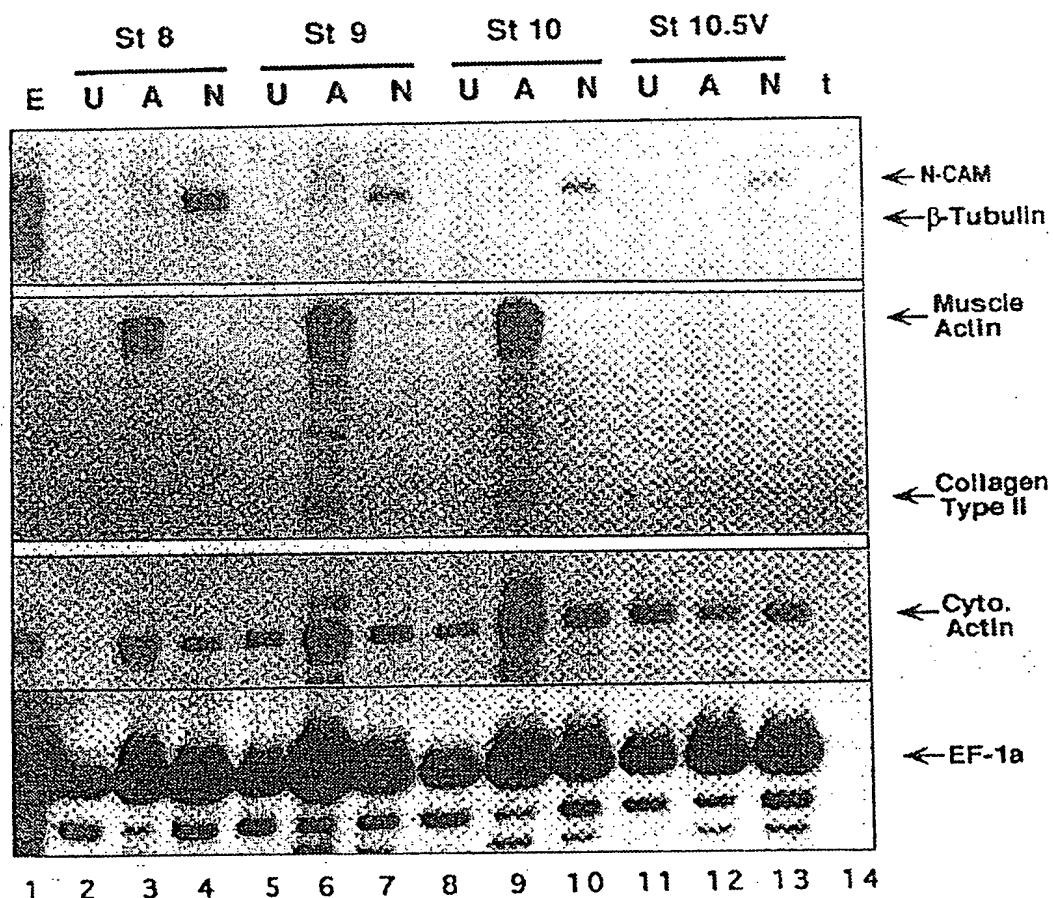
Fig. 3.



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Fig. 4A.



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Fig. 4B.

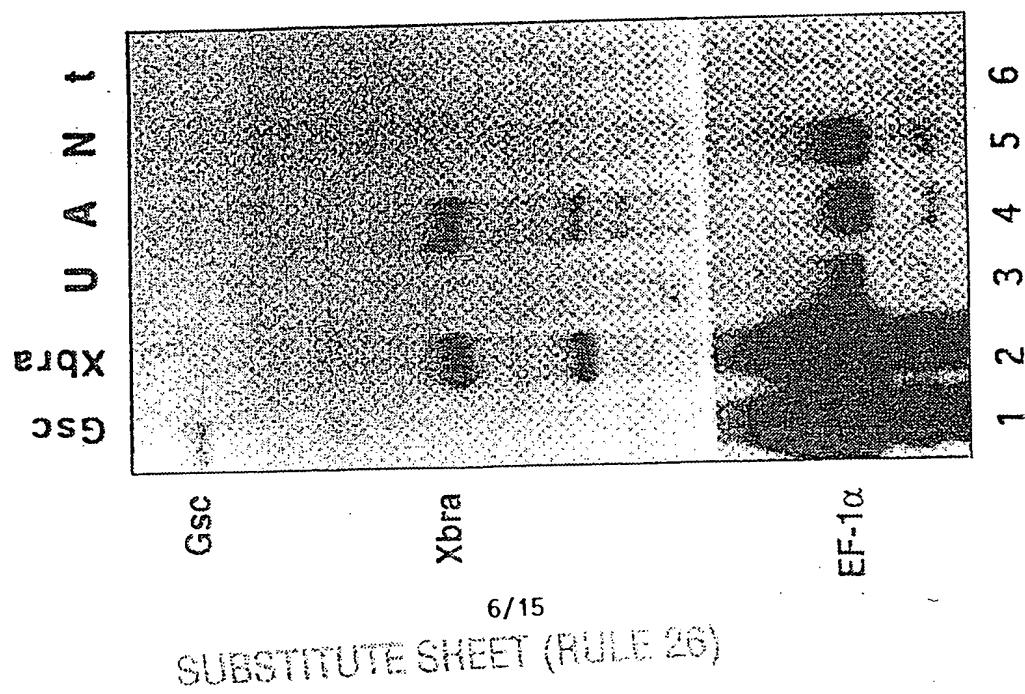


Fig. 4C.

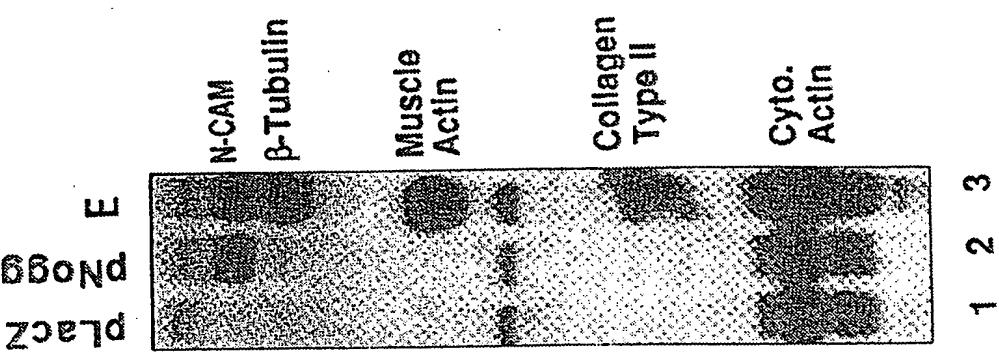
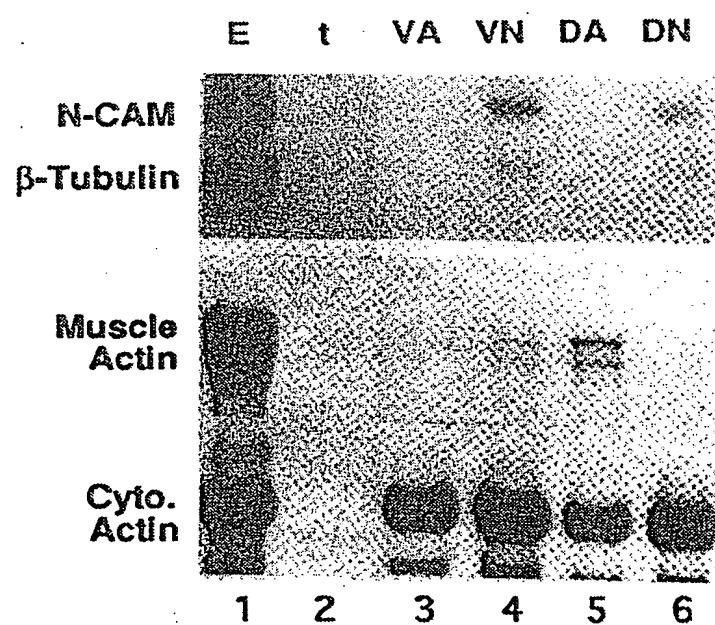


Fig.5.

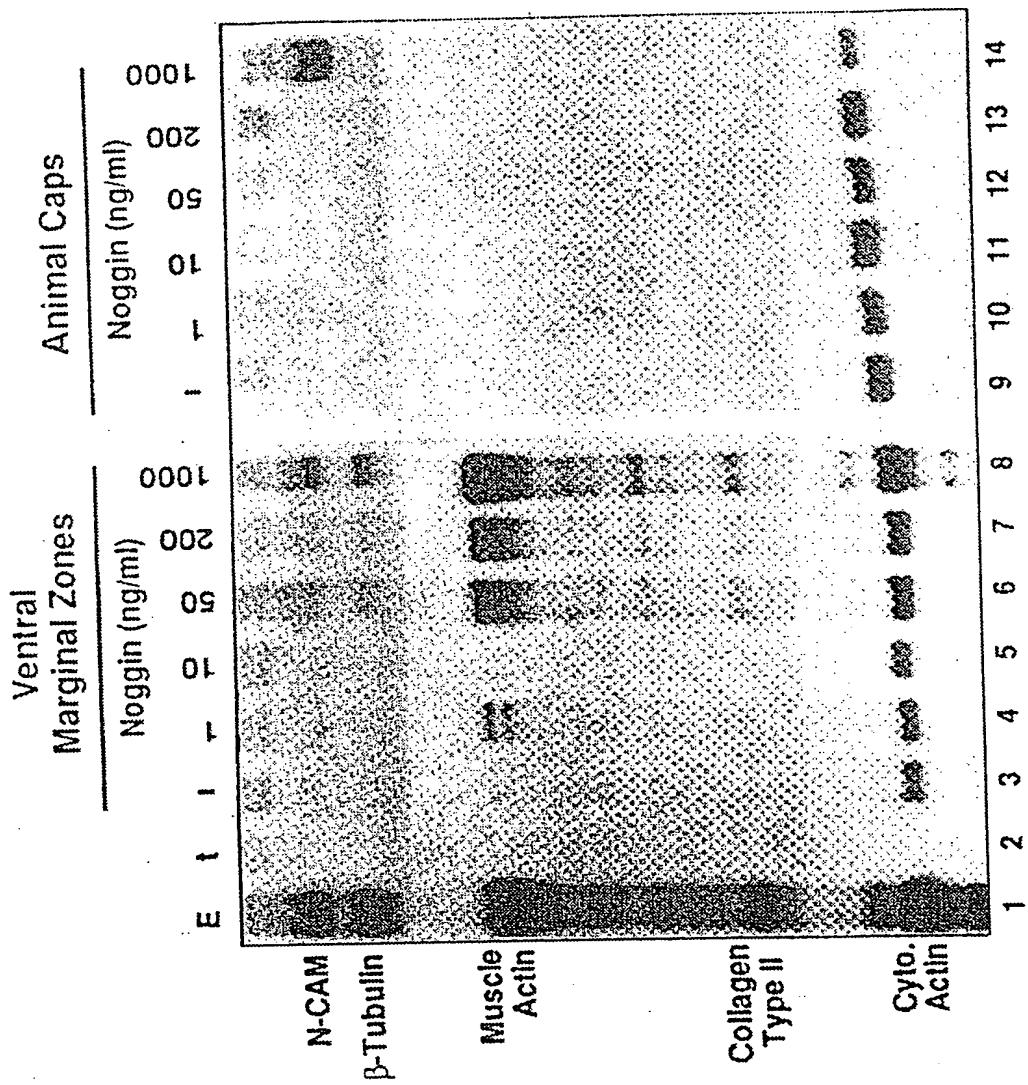


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Fig. 6.



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Fig. 7A.

N-CAM

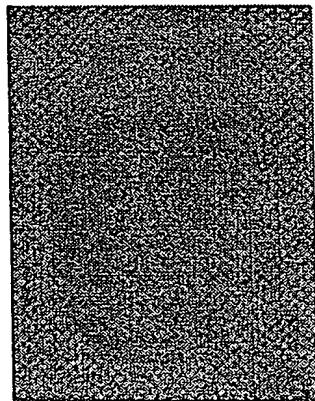


Fig. 7B.

N-CAM

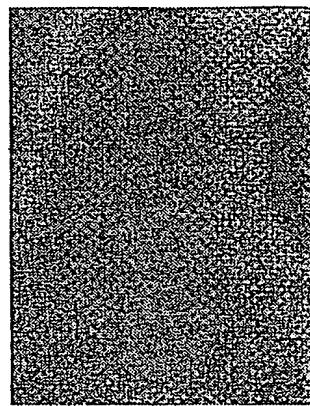


Fig. 7C

## Muscle Actin

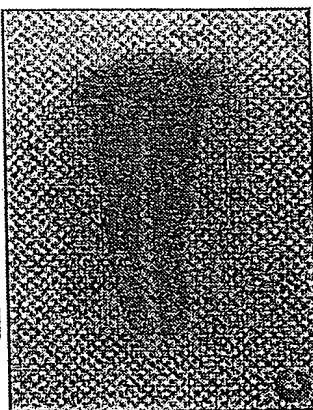
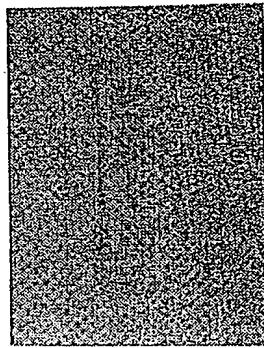


Fig.7D.

Embryo



6F11

Fig.7E.

+ Noggin

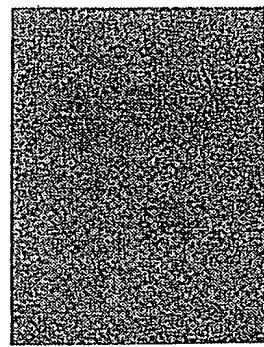
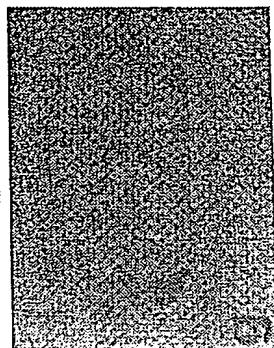


Fig.7G.



XAG

Fig.7F.

Untreated

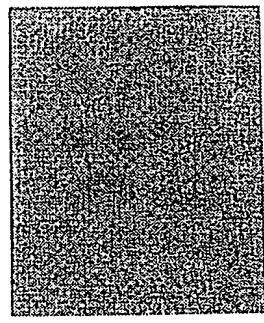


Fig.7I.

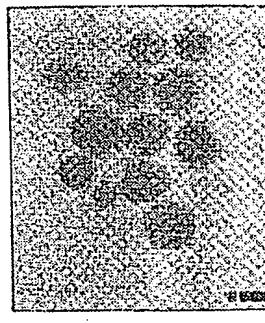


Fig.7L.

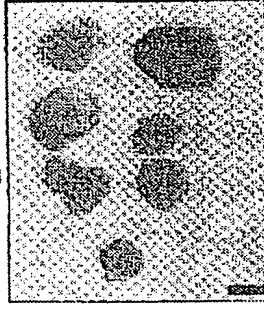


Fig.7K.

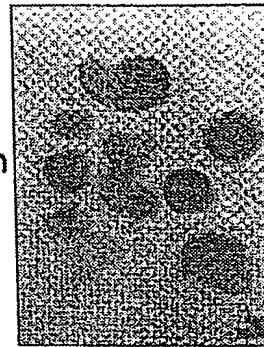
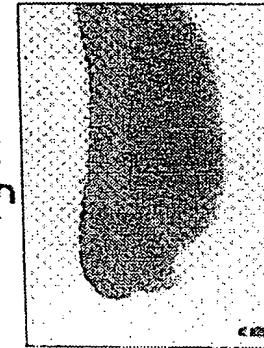


Fig.7J.



OTX

DISSEMINATION

Fig. 8.

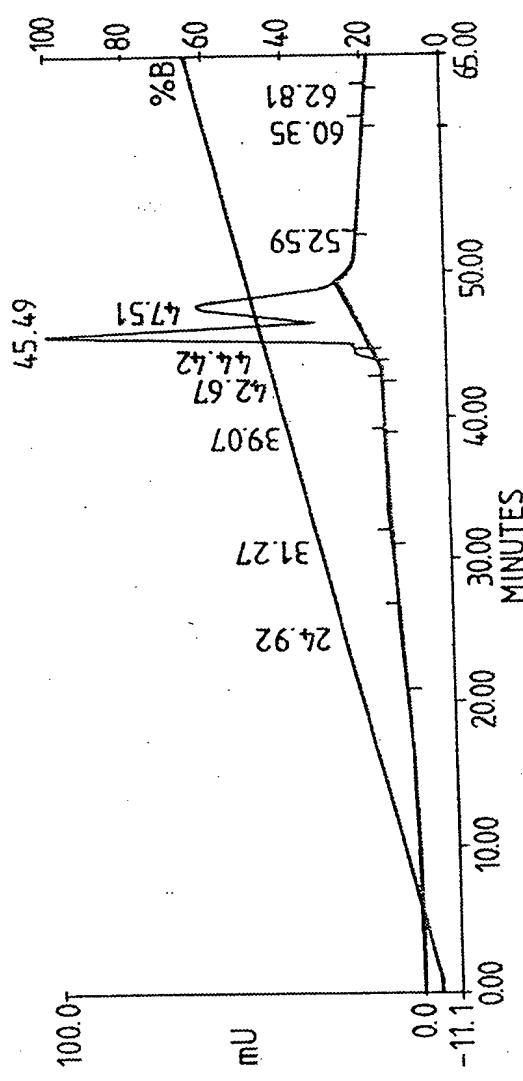


Fig. 9.

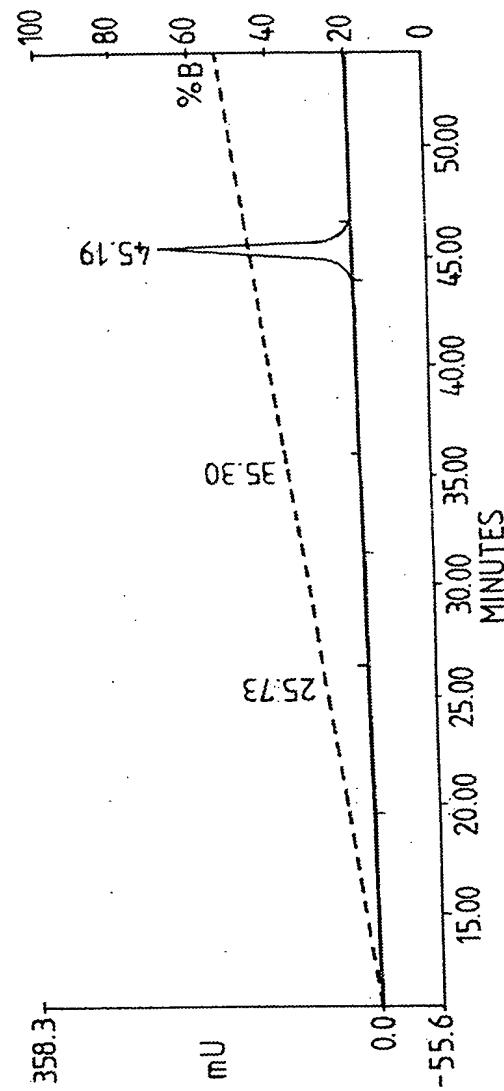


Fig.10

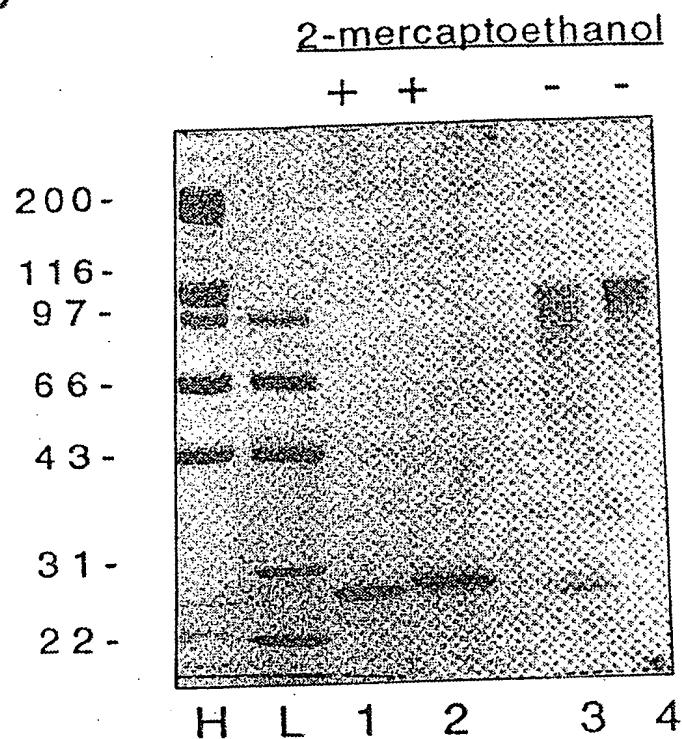
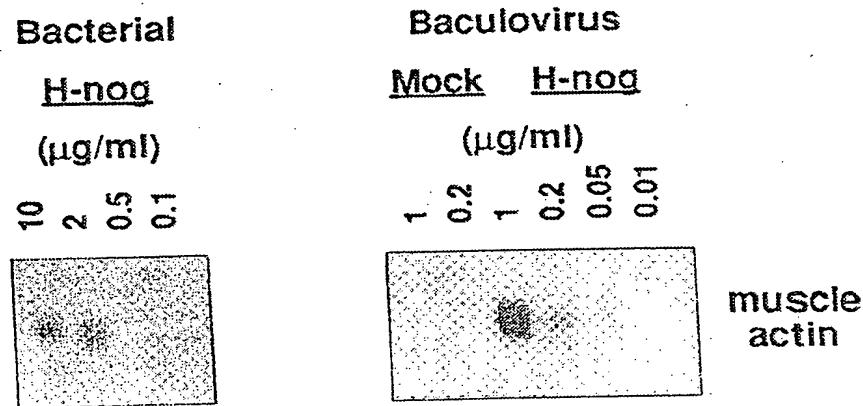


Fig.12:



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Fig. 11.

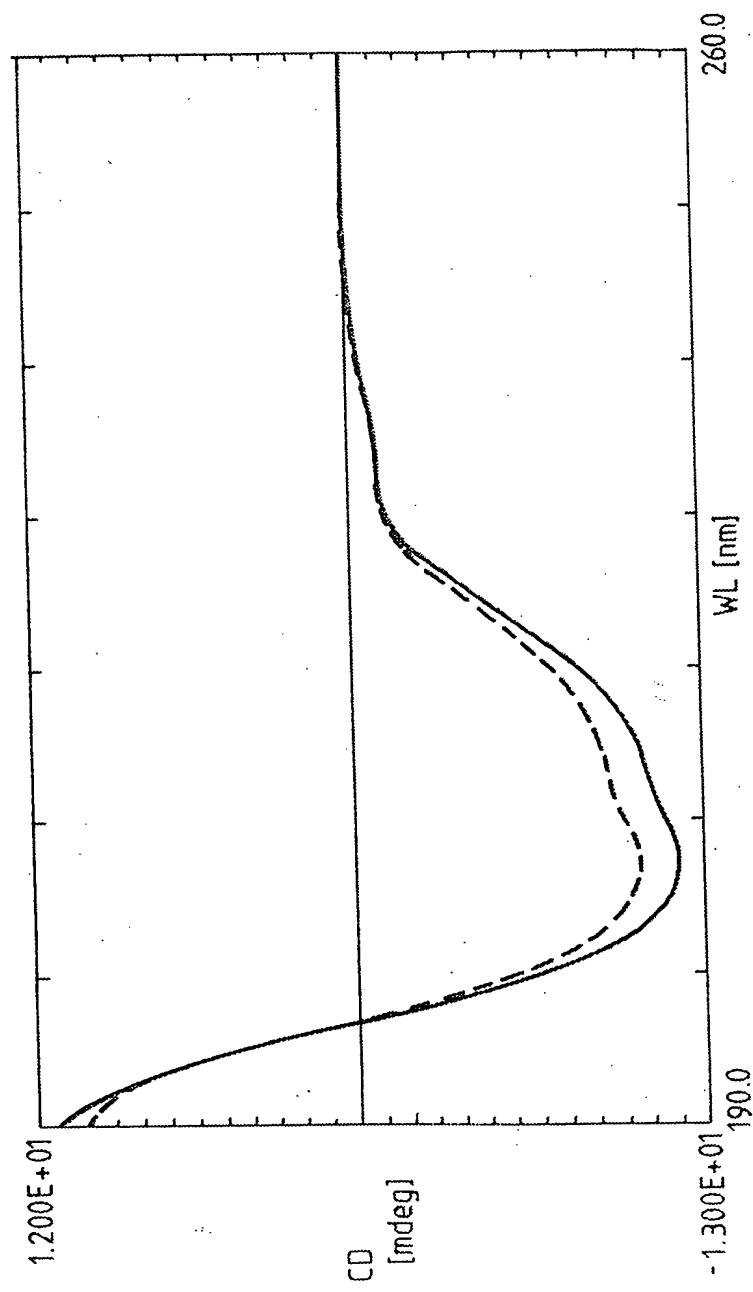


Fig.13.

5	10	15	20	25	30	35	40	45	50	55	60
TAACTCACTC ATTAGNCACC CCAGCCTTAC ACITTTATGCT TCCGGCTCGT ATGTTGTGTG											
65	70	75	80	85	90	95	100	105	110	115	120
GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA TGACCATGAT TACGCCAAGC											
125	130	135	140	145	150	155	160	165	170	175	180
TCGAAATTAA CCCTCACTAA AGGGAACAAA AGCTGGAGCT CCACCGCGGT GGCAGGCC											
185	190	195	200	205	210	215	220	225	230	235	240
TTCCCAAGTA GAGCCGGCGGG GGGGAATTGC GACCAACTCG TGCGCGTCTT CTGCAGCC											
245	250	255	260	265	270	275	280	285	290	295	300
GCGGGAGCCG GCGCTGCGCG AACGGCTCTC CTCGCAGCTC ATGCTGCCTG CCCTGGCC											
305	310	315	320	325	330	335	340	345	350	355	360
GCTCAGCCCTC GGCTGAGCCA CCTCCGGAGG GACCGGGGAG CGCGGCAGCG CGCGGGACTC											
365	370	375	380	385	390	395	400	405	410	415	420
GGCGTGCCTC CCTCCGGGGA CGCGGGAGCA AGAGGGAGCC CCCGGGGCGCG CGCGGGAGGC											
425	430	435	440	445	450	455	460	465	470	475	480
ATGGAGGCCT GCCCCAGCCT GGGGGTCACC CTCTACGCCG TGTTGGTGGT CCTGGGGCTG											
M	E	R	C	P	S	L	G	V	T	L	Y
485	490	495	500	505	510	515	520	525	530	535	540
A C G G C A C C A G C C G G C G G C C A G C A T A T C C G C C A G C A C C C A G C G A C A A C											
R	A	A	P	A	G	G	Q	H	Y	L	H
545	550	555	560	565	570	575	580	585	590	595	600
CTGCCCTGG TGGACCTCAT CGAACATCCA GACCTATCT TTGACCCCTAA GGAGAAGGAT											
L	P	L	V	D	L	I	E	H	P	D	P
605	610	615	620	625	630	635	640	645	650	655	660
CTGAACGAGA CGCTGCTGCG CTCGCTGCTC GGGGGCCACT ACGACCCGGG CTTTATGGCC											
L	N	E	T	L	L	R	S	L	L	G	H
665	670	675	680	685	690	695	700	705	710	715	720
ACITTCGCCCT CAGAGGACCG ACCCGGAGGG GGCAGGGGAC CGGCTGGAGG TGCCGAGGAC											
T	S	P	P	E	D	R	P	G	G	G	G
725	730	735	740	745	750	755	760	765	770	775	780
CTGGCGGAGC TGGACCAAGCT GCTGCAGCAG CGGCGCTCGG GGGCCATGCC GAGCCAGATC											
L	A	E	L	D	Q	L	L	R	Q	R	P
785	790	795	800	805	810	815	820	825	830	835	840

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Fig.13.(cont.)

AAAGGGCTGG	AGTTCTCCGA	GGGCTTGGCC	CAAGGCAAGA	AACAGCGCCT	GACCAAGAAG
K G L	E F S E	G L A	Q G K	K Q R L	S K K>
845 850	855 860	865 870	875 880	885 890	895 900
*	*	*	*	*	*
CTGAGGGAGGA	AGTTACAGAT	GTGGCTGTGG	TCACAGACCT	TCTGCCCGGT	GCTGTACCGG
L R R	K L Q M	W L W	S Q T	F C P V	L Y A>
905 910	915 920	925 930	935 940	945 950	955 960
*	*	*	*	*	*
TGGAATGACC	TAGGCAGCCG	CTTTTGGCCA	CGCTACGTGA	AGGTGGGCAG	CTGCTTCAGC
W N D	L G S R	F W P	R Y V	K V G S	C F S>
965 970	975 980	985 990	995 1000	1005 1010	1015 1020
*	*	*	*	*	*
AAGCGCTCCCT	GCTCTGTGCC	CGAGGGCATG	GTGTGTAAGC	CATCCAAGTC	TGTGCACCTC
K R S	C S V P	E G M	V C K	P S K S	V H L>
1025 1030	1035 1040	1045 1050	1055 1060	1065 1070	1075 1080
*	*	*	*	*	*
ACGGTGTGCTGC	GGTGGCGCTG	TCAGCGGCCG	GGGGGTCAAGC	GCTGCCGCTG	GATTCCCACATC
T V L	R W R C	Q R R	G G Q	R C G W	I P I>
1085 1090	1095 1100	1105 1110	1115 1120	1125 1130	1135 1140
*	*	*	*	*	*
CAGTACCCCCA	TCATTTCCGA	GTGTAAGTGT	TCCTGCTAGA	ACTCGGGGGG	GGCCCCCTGCC
Q Y P	I I S E	C K C	S C >>		
1145 1150	1155 1160	1165 1170	1175 1180		
*	*	*	*		
CGCGCCCCAGA	CACTTGATGG	ATCCCCGGGG	CTGAGATTTT		